

1/36

SEQUENCE LISTING

<110> Institut Pasteur
 Roche Diagnostics GmbH
 Pharma-Waldhof GmbH & Co.KG

<120> Enzymatic synthesis of deoxyribonucleosides

<130> 20373PWO Deoxyribonucleosides

<140>
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<150> EP99116425.2
 <151> 1999-08-20

<160> 20

<170> PatentIn Ver. 2.1

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 <213> Escherichia coli

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act atc tcc gaa ggg cag att gcc gcc ctc gcg atg acc att ttc ttc 144
 Thr Ile Ser Glu Gly Gln Ile Ala Ala Leu Ala Met Thr Ile Phe Phe
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cac gat atg aca atg cct gag cgt gtc tcg ctg acc atg gcg atg cga	192
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Asp Ser Gly Thr Val Leu Asp Trp Lys Ser Leu His Leu Asn Gly Pro	
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Ile Val Asp Lys His Ser Thr Gly Gly Val Gly Asp Val Thr Ser Leu	
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Met Leu Gly Pro Met Val Ala Ala Cys Gly Gly Tyr Ile Pro Met Ile	
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Ser Gly Arg Gly Leu Gly His Thr Gly Gly Thr Leu Asp Lys Leu Glu	
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Ser Ile Pro Gly Phe Asp Ile Phe Pro Asp Asp Asn Arg Phe Arg Glu
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Ala Phe Met Pro Thr Tyr Glu Leu Ser Glu Ala Leu Ala Glu Ala Ile
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Val Gly Val Ala Asn Gly Ala Gly Val Arg Thr Thr Ala Leu Leu Thr
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Asp Met Asn Gln Val Leu Ala Ser Ser Ala Gly Asn Ala Val Glu Val
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Arg Glu Ala Val Gln Phe Leu Thr Gly Glu Tyr Arg Asn Pro Arg Leu
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Phe Asp Val Thr Met Ala Leu Cys Val Glu Met Leu Ile Ser Gly Lys
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Glu Met Asp Thr Arg Ala Leu Gly Met Ala Val Val Ala Met Gly Gly
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Val Ile His Ala Lys Asp Glu Asn Asn Trp Gln Glu Ala Ala Lys Ala
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Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Ala Cys Thr	
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Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala	
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Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala	
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Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile	
165 170 175	
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Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu	
180 185 190	
ttt ggc gcg aaa gcc ctg acc atc tgc acc gta tct gac cac atc cgc	624
Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg	
195 200 205	
act cac gag cag acc act gcc gct gag cgt cag act acc ttc aac gac	672
Thr His Glu Gln Thr Thr Ala Ala Glu Arg Gln Thr Thr Phe Asn Asp	
210 215 220	
atg atc aaa atc gca ctg gaa tcc gtt ctg ctg ggc gat aaa gag taa	720
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 Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly
 50 55 60
 Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp
 65 70 75 80
 Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu
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 Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Ala Cys Thr
 100 105 110
 Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala
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 Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala
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 Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile
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 Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg
 195 200 205
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His Ile Ala Glu Ala Cys Ala Lys Gly Glu Ala Asp Asn Gly Arg Lys
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ggc ccg ctc aat ctg cca aat ctg acc cgt ctg ggg ctg gcg aaa gca   192
Gly Pro Leu Asn Leu Pro Asn Leu Thr Arg Leu Gly Leu Ala Lys Ala
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cac gaa ggt tct acc ggt ttc att ccg gcg gga atg gac ggc aac gct   240
His Glu Gly Ser Thr Gly Phe Ile Pro Ala Gly Met Asp Gly Asn Ala
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gaa gtt atc ggc gcg tac gca tgg gcg cac gaa atg tca tcc ggt aaa   288
Glu Val Ile Gly Ala Tyr Ala Trp Ala His Glu Met Ser Ser Gly Lys
           85             90             95

gat acc ccg tct ggt cac tgg gaa att gcc ggt gtc ccg gtt ctg ttt   336
Asp Thr Pro Ser Gly His Trp Glu Ile Ala Gly Val Pro Val Leu Phe
           100            105            110

gag tgg gga tat ttc tcc gat cac gaa aac agc ttc ccg caa gag ctg   384
Glu Trp Gly Tyr Phe Ser Asp His Glu Asn Ser Phe Pro Gln Glu Leu
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tgc cac tct tcc ggt acg gtc att ctg gat caa ctg ggc gaa gag cac	480
Cys His Ser Ser Gly Thr Val Ile Leu Asp Gln Leu Gly Glu Glu His	
145 150 155 160	
atg aaa acc ggc aag ccg att ttc tat acc tcc gct gac tcc gtg ttc	528
Met Lys Thr Gly Lys Pro Ile Phe Tyr Thr Ser Ala Asp Ser Val Phe	
165 170 175	
cag att gcc tgc cat gaa gaa act ttc ggt ctg gat aaa ctg tac gaa	576
Gln Ile Ala Cys His Glu Glu Thr Phe Gly Leu Asp Lys Leu Tyr Glu	
180 185 190	
ctg tgc gaa atc gcc cgt gaa gag ctg acc aac ggc ggc tac aat atc	624
Leu Cys Glu Ile Ala Arg Glu Glu Leu Thr Asn Gly Gly Tyr Asn Ile	
195 200 205	
ggg cgt gtt atc gct cgt ccg ttt atc ggc gac aaa gcc ggt aac ttc	672
Gly Arg Val Ile Ala Arg Pro Phe Ile Gly Asp Lys Ala Gly Asn Phe	
210 215 220	
cag cgt acc ggt aac cgt cac gac ctg gct gtt gag ccg cca gca ccg	720
Gln Arg Thr Gly Asn Arg His Asp Leu Ala Val Glu Pro Pro Ala Pro	
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acc gtg ctg cag aaa ctg gtt gat gaa aaa cac ggc cag gtg gtt tct	768
Thr Val Leu Gln Lys Leu Val Asp Glu Lys His Gly Gln Val Val Ser	
245 250 255	
gtc ggt aaa att gcg gac atc tac gcc aac tgc ggt atc acc aaa aaa	816
Val Gly Lys Ile Ala Asp Ile Tyr Ala Asn Cys Gly Ile Thr Lys Lys	
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gtg aaa gcg act ggc ctg gac gcg ctg ttt gac gcc acc atc aaa gag	864
Val Lys Ala Thr Gly Leu Asp Ala Leu Phe Asp Ala Thr Ile Lys Glu	
275 280 285	
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Met Lys Glu Ala Gly Asp Asn Thr Ile Val Phe Thr Asn Phe Val Asp	
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 325 330 335

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 Thr Trp Thr Gly Thr Asp His Thr Arg Glu His Ile Pro Val Leu Val
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His Glu Gly Ser Thr Gly Phe Ile Pro Ala Gly Met Asp Gly Asn Ala
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Asp Thr Pro Ser Gly His Trp Glu Ile Ala Gly Val Pro Val Leu Phe
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Glu Trp Gly Tyr Phe Ser Asp His Glu Asn Ser Phe Pro Gln Glu Leu
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Leu Asp Lys Leu Val Glu Arg Ala Asn Leu Pro Gly Tyr Leu Gly Asn
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Cys His Ser Ser Gly Thr Val Ile Leu Asp Gln Leu Gly Glu Glu His
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Gln Ile Ala Cys His Glu Glu Thr Phe Gly Leu Asp Lys Leu Tyr Glu
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Gly Arg Val Ile Ala Arg Pro Phe Ile Gly Asp Lys Ala Gly Asn Phe
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Gln Arg Thr Gly Asn Arg His Asp Leu Ala Val Glu Pro Pro Ala Pro
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Thr Val Leu Gln Lys Leu Val Asp Glu Lys His Gly Gln Val Val Ser
 245 250 255

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Cys His Gln Ala Lys Thr Pro Val Gly Asn Thr Ala Ala Ile Cys Ile	
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acc ccg gaa atc cgt atc gct acg gta acc aac ttc cca cac ggt aac	240
Thr Pro Glu Ile Arg Ile Ala Thr Val Thr Asn Phe Pro His Gly Asn	
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Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala	
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Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala	
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 225 230 235 240

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Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala
 115 120 125

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Gly Val Glu Lys Thr Val Gly Phe Lys Pro Ala Gly Gly Val Arg Thr
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 Met Ser Lys Ile Phe Asp Phe Val Lys Pro Gly Val Ile Thr Gly Asp
 1 5 10 15

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gac gta cag aaa gtt ttc cag gta gca aaa gaa aac aac ttc gca ctg	96
Asp Val Gln Lys Val Phe Gln Val Ala Lys Glu Asn Asn Phe Ala Leu	
20 25 30	
cca gca gta aac tgc gtc ggt act gac tcc atc aac gcc gta ctg gaa	144
Pro Ala Val Asn Cys Val Gly Thr Asp Ser Ile Asn Ala Val Leu Glu	
35 40 45	
acc gct gct aaa gtt aaa gcg ccg gtt atc gtt cag ttc tcc aac ggt	192
Thr Ala Ala Lys Val Lys Ala Pro Val Ile Val Gln Phe Ser Asn Gly	
50 55 60	
ggg gct tcc ttt atc gct ggt aaa ggc gtg aaa tct gac gtt ccg cag	240
Gly Ala Ser Phe Ile Ala Gly Lys Gly Val Lys Ser Asp Val Pro Gln	
65 70 75 80	
ggg gct gct atc ctg ggc gcg atc tct ggt gcg cat cac gtt cac cag	288
Gly Ala Ala Ile Leu Gly Ala Ile Ser Gly Ala His His Val His Gln	
85 90 95	
atg gct gaa cat tat ggt gtt ccg gtt atc ctg cac act gac cac tgc	336
Met Ala Glu His Tyr Gly Val Pro Val Ile Leu His Thr Asp His Cys	
100 105 110	
gcg aag aaa ctg ctg ccg tgg atc gac ggt ctg ttg gac gcg ggt gaa	384
Ala Lys Lys Leu Leu Pro Trp Ile Asp Gly Leu Leu Asp Ala Gly Glu	
115 120 125	
aaa cac ttc gca gct acc ggt aag ccg ctg ttc tct tct cac atg atc	432
Lys His Phe Ala Ala Thr Gly Lys Pro Leu Phe Ser Ser His Met Ile	
130 135 140	
gac ctg tct gaa gaa tct ctg caa gag aac atc gaa atc tgc tct aaa	480
Asp Leu Ser Glu Glu Ser Leu Gln Glu Asn Ile Glu Ile Cys Ser Lys	
145 150 155 160	
tac ctg gag cgc atg tcc aaa atc ggc atg act ctg gaa atc gaa ctg	528
Tyr Leu Glu Arg Met Ser Lys Ile Gly Met Thr Leu Glu Ile Glu Leu	
165 170 175	
ggg tgc acc ggt ggt gaa gaa gac ggc gtg gac aac agc cac atg gac	576
Gly Cys Thr Gly Gly Glu Glu Asp Gly Val Asp Asn Ser His Met Asp	
180 185 190	

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gct tct gca ctg tac acc cag ccg gaa gac gtt gat tac gca tac acc	624
Ala Ser Ala Leu Tyr Thr Gln Pro Glu Asp Val Asp Tyr Ala Tyr Thr	
195 200 205	
 gaa ctg agc aaa atc agc ccg cgt ttc acc atc gca gcg tcc ttc ggt	672
Glu Leu Ser Lys Ile Ser Pro Arg Phe Thr Ile Ala Ala Ser Phe Gly	
210 215 220	
 aac gta cac ggt gtt tac aag ccg ggt aac gtg gtt ctg act ccg acc	720
Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Val Leu Thr Pro Thr	
225 230 235 240	
 atc ctg cgt gat tct cag gaa tat gtt tcc aag aaa cac aac ctg ccg	768
Ile Leu Arg Asp Ser Gln Glu Tyr Val Ser Lys Lys His Asn Leu Pro	
245 250 255	
 cac aac agc ctg aac ttc gta ttc cac ggt ggt tcc ggt tct act gct	816
His Asn Ser Leu Asn Phe Val Phe His Gly Gly Ser Gly Ser Thr Ala	
260 265 270	
 cag gaa atc aaa gac tcc gta agc tac ggc gta gta aaa atg aac atc	864
Gln Glu Ile Lys Asp Ser Val Ser Tyr Gly Val Val Lys Met Asn Ile	
275 280 285	
 gat acc gat acc caa tgg gca acc tgg gaa ggc gtt ctg aac tac tac	912
Asp Thr Asp Thr Gln Trp Ala Thr Trp Glu Gly Val Leu Asn Tyr Tyr	
290 295 300	
 aaa gcg aac gaa gct tat ctg cag ggt cag ctg ggt aac ccg aaa ggc	960
Lys Ala Asn Glu Ala Tyr Leu Gln Gly Gln Leu Gly Asn Pro Lys Gly	
305 310 315 320	
 gaa gat cag ccg aac aag aaa tac tac gat ccg cgc gta tgg ctg cgt	1008
Glu Asp Gln Pro Asn Lys Lys Tyr Tyr Asp Pro Arg Val Trp Leu Arg	
325 330 335	
 gcc ggt cag act tcg atg atc gct cgt ctg gag aaa gca ttc cag gaa	1056
Ala Gly Gln Thr Ser Met Ile Ala Arg Leu Glu Lys Ala Phe Gln Glu	
340 345 350	
 ctg aac gcg atc gac gtt ctg taa	1080
Leu Asn Ala Ile Asp Val Leu	
355	

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<210> 10

<211> 359

<212> PRT

<213> Escherichia coli

<400> 10

Met Ser Lys Ile Phe Asp Phe Val Lys Pro Gly Val Ile Thr Gly Asp
 1 5 10 15

Asp Val Gln Lys Val Phe Gln Val Ala Lys Glu Asn Asn Phe Ala Leu
 20 25 30

Pro Ala Val Asn Cys Val Gly Thr Asp Ser Ile Asn Ala Val Leu Glu
 35 40 45

Thr Ala Ala Lys Val Lys Ala Pro Val Ile Val Gln Phe Ser Asn Gly
 50 55 60

Gly Ala Ser Phe Ile Ala Gly Lys Gly Val Lys Ser Asp Val Pro Gln
 65 70 75 80

Gly Ala Ala Ile Leu Gly Ala Ile Ser Gly Ala His His Val His Gln
 85 90 95

Met Ala Glu His Tyr Gly Val Pro Val Ile Leu His Thr Asp His Cys
 100 105 110

Ala Lys Lys Leu Leu Pro Trp Ile Asp Gly Leu Leu Asp Ala Gly Glu
 115 120 125

Lys His Phe Ala Ala Thr Gly Lys Pro Leu Phe Ser Ser His Met Ile
 130 135 140

Asp Leu Ser Glu Glu Ser Leu Gln Glu Asn Ile Glu Ile Cys Ser Lys
 145 150 155 160

Tyr Leu Glu Arg Met Ser Lys Ile Gly Met Thr Leu Glu Ile Glu Leu
 165 170 175

Gly Cys Thr Gly Gly Glu Glu Asp Gly Val Asp Asn Ser His Met Asp
 180 185 190

Ala Ser Ala Leu Tyr Thr Gln Pro Glu Asp Val Asp Tyr Ala Tyr Thr
 195 200 205

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Glu Leu Ser Lys Ile Ser Pro Arg Phe Thr Ile Ala Ala Ser Phe Gly
 210 215 220

Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Val Leu Thr Pro Thr
 225 230 235 240

Ile Leu Arg Asp Ser Gln Glu Tyr Val Ser Lys Lys His Asn Leu Pro
 245 250 255

His Asn Ser Leu Asn Phe Val Phe His Gly Gly Ser Gly Ser Thr Ala
 260 265 270

Gln Glu Ile Lys Asp Ser Val Ser Tyr Gly Val Val Lys Met Asn Ile
 275 280 285

Asp Thr Asp Thr Gln Trp Ala Thr Trp Glu Gly Val Leu Asn Tyr Tyr
 290 295 300

Lys Ala Asn Glu Ala Tyr Leu Gln Gly Gln Leu Gly Asn Pro Lys Gly
 305 310 315 320

Glu Asp Gln Pro Asn Lys Lys Tyr Tyr Asp Pro Arg Val Trp Leu Arg
 325 330 335

Ala Gly Gln Thr Ser Met Ile Ala Arg Leu Glu Lys Ala Phe Gln Glu
 340 345 350

Leu Asn Ala Ile Asp Val Leu
 355

<210> 11

<211> 921

<212> DNA

<213> Salmonella typhi

<220>

<221> CDS

<222> (1)..(918)

<400> 11

atg gat atc gcg gtt att ggc tct aac atg gtg gac ctt atc acc tac 48
 Met Asp Ile Ala Val Ile Gly Ser Asn Met Val Asp Leu Ile Thr Tyr
 1 5 10 15

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acc aac cag atg ccc aaa gaa ggg gaa act ctg gaa gcg ccg gcg ttt	96
Thr Asn Gln Met Pro Lys Glu Gly Glu Thr Leu Glu Ala Pro Ala Phe	
20 25 30	
aaa atc ggc tgc ggc gga aaa ggg gcg aac cag gcc gtg gcg gcc gct	144
Lys Ile Gly Cys Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala	
35 40 45	
aag ctc aat tca aaa gta ttg atg ttg acc aaa gtg ggc gac gat att	192
Lys Leu Asn Ser Lys Val Leu Met Leu Thr Lys Val Gly Asp Asp Ile	
50 55 60	
ttt gcc gac aac acc att cgt aat ctc gaa tcc tgg ggg atc aat acg	240
Phe Ala Asp Asn Thr Ile Arg Asn Leu Glu Ser Trp Gly Ile Asn Thr	
65 70 75 80	
acg tat gta gaa aaa gta ccg tgt acc agc agc ggc gta gcg ccg att	288
Thr Tyr Val Glu Lys Val Pro Cys Thr Ser Ser Gly Val Ala Pro Ile	
85 90 95	
ttc gtc aac gcc aac tcc agc aac agc att ctg atc atc aaa ggc gct	336
Phe Val Asn Ala Asn Ser Ser Asn Ser Ile Leu Ile Ile Lys Gly Ala	
100 105 110	
aac aag ttt ctc tcg ccg gaa gat atc gat cgc gcg gcg gaa gat tta	384
Asn Lys Phe Leu Ser Pro Glu Asp Ile Asp Arg Ala Ala Glu Asp Leu	
115 120 125	
aaa aaa tgc cag ctt att gtt ctg caa ctg gaa gtt cag ctt gaa acg	432
Lys Lys Cys Gln Leu Ile Val Leu Gln Leu Glu Val Gln Leu Glu Thr	
130 135 140	
gtt tat cac gca ata gaa ttt ggc aag aaa cac ggg att gaa gtg tta	480
Val Tyr His Ala Ile Glu Phe Gly Lys Lys His Gly Ile Glu Val Leu	
145 150 155 160	
tta aac cct gcg cca gca tta cgg gaa tta gat atg tct tat gcc tgt	528
Leu Asn Pro Ala Pro Ala Leu Arg Glu Leu Asp Met Ser Tyr Ala Cys	
165 170 175	
aaa tgc gat ttc ttt gta cct aat gaa acc gag ctg gaa ata tta acc	576
Lys Cys Asp Phe Phe Val Pro Asn Glu Thr Glu Leu Glu Ile Leu Thr	
180 185 190	

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ggt atg cca gtg gat acc tat gac cat att cgc gca gcg gca cgt tcg 624
 Gly Met Pro Val Asp Thr Tyr Asp His Ile Arg Ala Ala Arg Ser
 195 200 205

ctg gta gat aaa ggg ctg aac aat att att gtc acc atg ggc gag aaa 672
 Leu Val Asp Lys Gly Leu Asn Asn Ile Ile Val Thr Met Gly Glu Lys
 210 215 220

ggc gcg ctg tgg atg acg cgt gac cag gaa gtc cat gtt ccg gcg ttt 720
 Gly Ala Leu Trp Met Thr Arg Asp Gln Glu Val His Val Pro Ala Phe
 225 230 235 240

aga gtg aac gct gtt gat acc agc ggc gcg ggc gat gcc ttt atc ggc 768
 Arg Val Asn Ala Val Asp Thr Ser Gly Ala Gly Asp Ala Phe Ile Gly
 245 250 255

tgt ttc gcg cat tac tac gtc cag agc ggg gat gtg gaa gcc gcc atg 816
 Cys Phe Ala His Tyr Tyr Val Gln Ser Gly Asp Val Glu Ala Ala Met
 260 265 270

aaa aaa gcc gtc ctc ttt gcc gct ttc agc gtc acc ggg aaa ggc acc 864
 Lys Lys Ala Val Leu Phe Ala Ala Phe Ser Val Thr Gly Lys Gly Thr
 275 280 285

caa tcc tct tat cca agc att gag caa ttt aat gag tat ctt tcg ttg 912
 Gln Ser Ser Tyr Pro Ser Ile Glu Gln Phe Asn Glu Tyr Leu Ser Leu
 290 295 300

aac gaa taa 921
 Asn Glu
 305

<210> 12

<211> 306

<212> PRT

<213> Salmonella typhi

<400> 12

Met Asp Ile Ala Val Ile Gly Ser Asn Met Val Asp Leu Ile Thr Tyr
 1 5 10 15

Thr Asn Gln Met Pro Lys Glu Gly Glu Thr Leu Glu Ala Pro Ala Phe
 20 25 30

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Lys Ile Gly Cys Gly Gly Lys Gly Ala Asn Gln Ala Val Ala Ala Ala
 35 40 45

Lys Leu Asn Ser Lys Val Leu Met Leu Thr Lys Val Gly Asp Asp Ile
 50 55 60

Phe Ala Asp Asn Thr Ile Arg Asn Leu Glu Ser Trp Gly Ile Asn Thr
 65 70 75 80

Thr Tyr Val Glu Lys Val Pro Cys Thr Ser Ser Gly Val Ala Pro Ile
 85 90 95

Phe Val Asn Ala Asn Ser Ser Asn Ser Ile Leu Ile Ile Lys Gly Ala
 100 105 110

Asn Lys Phe Leu Ser Pro Glu Asp Ile Asp Arg Ala Ala Glu Asp Leu
 115 120 125

Lys Lys Cys Gln Leu Ile Val Leu Gln Leu Glu Val Gln Leu Glu Thr
 130 135 140

Val Tyr His Ala Ile Glu Phe Gly Lys Lys His Gly Ile Glu Val Leu
 145 150 155 160

Leu Asn Pro Ala Pro Ala Leu Arg Glu Leu Asp Met Ser Tyr Ala Cys
 165 170 175

Lys Cys Asp Phe Phe Val Pro Asn Glu Thr Glu Leu Glu Ile Leu Thr
 180 185 190

Gly Met Pro Val Asp Thr Tyr Asp His Ile Arg Ala Ala Ala Arg Ser
 195 200 205

Leu Val Asp Lys Gly Leu Asn Asn Ile Ile Val Thr Met Gly Glu Lys
 210 215 220

Gly Ala Leu Trp Met Thr Arg Asp Gln Glu Val His Val Pro Ala Phe
 225 230 235 240

Arg Val Asn Ala Val Asp Thr Ser Gly Ala Gly Asp Ala Phe Ile Gly
 245 250 255

Cys Phe Ala His Tyr Tyr Val Gln Ser Gly Asp Val Glu Ala Ala Met
 260 265 270

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Lys Lys Ala Val Leu Phe Ala Ala Phe Ser Val Thr Gly Lys Gly Thr
 275 280 285

Gln Ser Ser Tyr Pro Ser Ile Glu Gln Phe Asn Glu Tyr Leu Ser Leu
 290 295 300

Asn Glu
 305

<210> 13

<211> 483

<212> DNA

<213> Lactobacillus leichmannii

<220>

<221> CDS

<222> (10) .. (480)

<400> 13

gtataactaa atg cca aaa aag acg atc tac ttc ggt gcc ggc tgg ttc act 51
 Met Pro Lys Lys Thr Ile Tyr Phe Gly Ala Gly Trp Phe Thr
 1 5 10

gac cgc caa aac aaa gcc tac aag gaa gcc atg gaa gcc ctc aag gaa 99
 Asp Arg Gln Asn Lys Ala Tyr Lys Glu Ala Met Glu Ala Leu Lys Glu
 15 20 25 30

aac cca acg att gac ctg gaa aac agc tac gtt ccc ctg gac aac cag 147
 Asn Pro Thr Ile Asp Leu Glu Asn Ser Tyr Val Pro Leu Asp Asn Gln
 35 40 45

tac aag ggt atc cgg gtt gat gaa cac ccg gaa tac ctg cat gac aag 195
 Tyr Lys Gly Ile Arg Val Asp Glu His Pro Glu Tyr Leu His Asp Lys
 50 55 60

gtt tgg gct acg gcc acc tac aac aac gac ttg aac ggg atc aag acc 243
 Val Trp Ala Thr Ala Thr Tyr Asn Asn Asp Leu Asn Gly Ile Lys Thr
 65 70 75

aac gac atc atg ctg ggt gtc tac atc cct gac gaa gaa gac gtc ggc 291
 Asn Asp Ile Met Leu Gly Val Tyr Ile Pro Asp Glu Glu Asp Val Gly
 80 85 90

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ctg ggc atg gaa ctg ggt tac gcc ttg agc caa ggc aag tac gtc ctt 339
 Leu Gly Met Glu Leu Gly Tyr Ala Leu Ser Gln Gly Lys Tyr Val Leu
 95 100 105 110

ttg gtc atc ccg gac gaa gac tac ggc aag ccg atc aac ctc atg agc 387
 Leu Val Ile Pro Asp Glu Asp Tyr Gly Lys Pro Ile Asn Leu Met Ser
 115 120 125

tgg ggc gtc agc gac aac gtg atc aag atg agc cag ctg aag gac ttc 435
 Trp Gly Val Ser Asp Asn Val Ile Lys Met Ser Gln Leu Lys Asp Phe
 130 135 140

aac ttc aac aag ccg cgc ttc gac ttc tac gaa ggt gcc gta tac taa 483
 Asn Phe Asn Lys Pro Arg Phe Asp Phe Tyr Glu Gly Ala Val Tyr
 145 150 155

<210> 14

<211> 157

<212> PRT

<213> Lactobacillus leichmannii

<400> 14

Met Pro Lys Lys Thr Ile Tyr Phe Gly Ala Gly Trp Phe Thr Asp Arg
 1 5 10 15

Gln Asn Lys Ala Tyr Lys Glu Ala Met Glu Ala Leu Lys Glu Asn Pro
 20 25 30

Thr Ile Asp Leu Glu Asn Ser Tyr Val Pro Leu Asp Asn Gln Tyr Lys
 35 40 45

Gly Ile Arg Val Asp Glu His Pro Glu Tyr Leu His Asp Lys Val Trp
 50 55 60

Ala Thr Ala Thr Tyr Asn Asn Asp Leu Asn Gly Ile Lys Thr Asn Asp
 65 70 75 80

Ile Met Leu Gly Val Tyr Ile Pro Asp Glu Glu Asp Val Gly Leu Gly
 85 90 95

Met Glu Leu Gly Tyr Ala Leu Ser Gln Gly Lys Tyr Val Leu Leu Val
 100 105 110

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Ile Pro Asp Glu Asp Tyr Gly Lys Pro Ile Asn Leu Met Ser Trp Gly
 115 120 125

Val Ser Asp Asn Val Ile Lys Met Ser Gln Leu Lys Asp Phe Asn Phe
 130 135 140

Asn Lys Pro Arg Phe Asp Phe Tyr Glu Gly Ala Val Tyr
 145 150 155

<210> 15

<211> 720

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(717)

<400> 15

atg gct acc cca cac att aat gca gaa atg ggc gat ttc gct gac gta 48
 Met Ala Thr Pro His Ile Asn Ala Glu Met Gly Asp Phe Ala Asp Val
 1 5 10 15

gtt ttg atg cca ggc gac ccg ctg cgt gcg aag tat att gct gaa act 96
 Val Leu Met Pro Gly Asp Pro Leu Arg Ala Lys Tyr Ile Ala Glu Thr
 20 25 30

ttc ctt gaa gat gcc cgt gaa gtg aac aac gtt cgc ggt atg ctg ggc 144
 Phe Leu Glu Asp Ala Arg Glu Val Asn Asn Val Arg Gly Met Leu Gly
 35 40 45

ttc acc ggt act tac aaa ggc cgc aaa att tcc gta atg ggt cac ggt 192
 Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly
 50 55 60

atg ggt atc ccg tcc tgc tcc atc tac acc aaa gaa ctg atc acc gat 240
 Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp
 65 70 75 80

ttc ggc gtg aag aaa att atc cgc gtg ggt tcc tgt ggc gca gtt ctg 288
 Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu
 85 90 95

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ccg cac gta aaa ctg cgc gac gtc gtt atc ggt atg ggt acc tgc acc 336
 Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Thr Cys Thr
 100 105 110

gat tcc aaa gtt aac cgc atc cgt ttt aaa gac cat gac ttt gcc gct 384
 Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala
 115 120 125

atc gct gac ttc gac atg gtg cgt aac gca gta gat gca gct aaa gca 432
 Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala
 130 135 140

ctg ggt att gat gct cgc gtg ggt aac ctg ttc tcc gct gac ctg ttc 480
 Leu Gly Ile Asp Ala Arg Val Gly Asn Leu Phe Ser Ala Asp Leu Phe
 145 150 155 160

tac tct ccg gac ggc gaa atg ttc gac gtg atg gaa aaa tac ggc att 528
 Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile
 165 170 175

ctc ggc gtg gaa atg gaa gcg gct ggt atc tac ggc gtc gct gca gaa 576
 Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu
 180 185 190

ttt ggc gcg aaa gcc ctg acc atc tgc acc gta tct gac cac atc cgc 624
 Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg
 195 200 205

act cac gag cag acc act gcc gct gag cgt cag act acc ttc aac aac 672
 Thr His Glu Gln Thr Thr Ala Ala Glu Arg Gln Thr Thr Phe Asn Asn
 210 215 220

atg atc aaa atc gca ctg gaa tcc gtt ctg ctg ggc gat aaa gag taa 720
 Met Ile Lys Ile Ala Leu Glu Ser Val Leu Leu Gly Asp Lys Glu
 225 230 235

<210> 16

<211> 239

<212> PRT

<213> Escherichia coli

<400> 16

Met Ala Thr Pro His Ile Asn Ala Glu Met Gly Asp Phe Ala Asp Val
 1 5 10 15

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Val Leu Met Pro Gly Asp Pro Leu Arg Ala Lys Tyr Ile Ala Glu Thr
 20 25 30

Phe Leu Glu Asp Ala Arg Glu Val Asn Asn Val Arg Gly Met Leu Gly
 35 40 45

Phe Thr Gly Thr Tyr Lys Gly Arg Lys Ile Ser Val Met Gly His Gly
 50 55 60

Met Gly Ile Pro Ser Cys Ser Ile Tyr Thr Lys Glu Leu Ile Thr Asp
 65 70 75 80

Phe Gly Val Lys Lys Ile Ile Arg Val Gly Ser Cys Gly Ala Val Leu
 85 90 95

Pro His Val Lys Leu Arg Asp Val Val Ile Gly Met Gly Thr Cys Thr
 100 105 110

Asp Ser Lys Val Asn Arg Ile Arg Phe Lys Asp His Asp Phe Ala Ala
 115 120 125

Ile Ala Asp Phe Asp Met Val Arg Asn Ala Val Asp Ala Ala Lys Ala
 130 135 140

Leu Gly Ile Asp Ala Arg Val Gly Asn Leu Phe Ser Ala Asp Leu Phe
 145 150 155 160

Tyr Ser Pro Asp Gly Glu Met Phe Asp Val Met Glu Lys Tyr Gly Ile
 165 170 175

Leu Gly Val Glu Met Glu Ala Ala Gly Ile Tyr Gly Val Ala Ala Glu
 180 185 190

Phe Gly Ala Lys Ala Leu Thr Ile Cys Thr Val Ser Asp His Ile Arg
 195 200 205

Thr His Glu Gln Thr Thr Ala Ala Glu Arg Gln Thr Thr Phe Asn Asn
 210 215 220

Met Ile Lys Ile Ala Leu Glu Ser Val Leu Leu Gly Asp Lys Glu
 225 230 235

<210> 17

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<211> 1224

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) .. (1221)

<400> 17

atg aaa cgt gca ttt att atg gtg ctg gac tca ttc ggc atc ggc gct	48
Met Lys Arg Ala Phe Ile Met Val Leu Asp Ser Phe Gly Ile Gly Ala	
1 5 10 15	
aca gaa gat gca gaa cgc ttt ggt gac gtc ggg gct gac acc ctg ggt	96
Thr Glu Asp Ala Glu Arg Phe Gly Asp Val Gly Ala Asp Thr Leu Gly	
20 25 30	
cat atc gca gaa gct tgt gcc aaa ggc gaa gct gat aac ggt cgt aaa	144
His Ile Ala Glu Ala Cys Ala Lys Gly Glu Ala Asp Asn Gly Arg Lys	
35 40 45	
ggc ccg ctc aat ctg cca aat ctg acc cgt ctg ggg ctg gcg aaa gca	192
Gly Pro Leu Asn Leu Pro Asn Leu Thr Arg Leu Gly Leu Ala Lys Ala	
50 55 60	
cac gaa ggt tct acc ggt ttc att ccg gcg gga atg gac ggc aac gct	240
His Glu Gly Ser Thr Gly Phe Ile Pro Ala Gly Met Asp Gly Asn Ala	
65 70 75 80	
gaa gtt atc ggc gcg tac gca tgg gcg cac gaa atg tca tcc ggt aaa	288
Glu Val Ile Gly Ala Tyr Ala Trp Ala His Glu Met Ser Ser Gly Lys	
85 90 95	
gat acc ccg tct ggt cac tgg gaa att gcc ggc gtc ccg gtt ctg ttt	336
Asp Thr Pro Ser Gly His Trp Glu Ile Ala Gly Val Pro Val Leu Phe	
100 105 110	
gag tgg gga tat ttc tcc gat cac gaa aac agc ttc ccg caa gag ctg	384
Glu Trp Gly Tyr Phe Ser Asp His Glu Asn Ser Phe Pro Gln Glu Leu	
115 120 125	
ctg gat aaa ctg gtc gaa cgc gct aat ctg ccg ggt tac ctc ggt aac	432
Leu Asp Lys Leu Val Glu Arg Ala Asn Leu Pro Gly Tyr Leu Gly Asn	
130 135 140	

tgc	cac	tct	tcc	ggg	acg	gtc	att	ctg	gat	caa	ctg	ggc	gaa	gag	cac	480
Cys	His	Ser	Ser	Gly	Thr	Val	Ile	Leu	Asp	Gln	Leu	Gly	Glu	Glu	His	
145					150					155					160	
atg	aaa	acc	ggc	aag	ccg	att	ttc	tat	acc	tcc	gct	gac	tcc	gtg	ttc	528
Met	Lys	Thr	Gly	Lys	Pro	Ile	Phe	Tyr	Thr	Ser	Ala	Asp	Ser	Val	Phe	
				165					170					175		
cag	att	gcc	tgc	cat	gaa	gaa	act	ttc	ggg	ctg	gat	aaa	ctc	tac	gaa	576
Gln	Ile	Ala	Cys	His	Glu	Glu	Thr	Phe	Gly	Leu	Asp	Lys	Leu	Tyr	Glu	
			180					185					190			
ctg	tgc	gaa	atc	gcc	cgt	gaa	gag	ctg	acc	aac	ggc	ggc	tac	aat	atc	624
Leu	Cys	Glu	Ile	Ala	Arg	Glu	Glu	Leu	Thr	Asn	Gly	Gly	Tyr	Asn	Ile	
		195					200					205				
ggg	cgt	gtt	atc	gct	cgt	ccg	ttt	atc	ggc	gac	aaa	gcc	ggg	aac	ttc	672
Gly	Arg	Val	Ile	Ala	Arg	Pro	Phe	Ile	Gly	Asp	Lys	Ala	Gly	Asn	Phe	
	210					215					220					
caa	cgt	acc	ggg	aac	cgt	cac	gac	ctg	gct	gtt	gag	ccg	cca	gca	ccg	720
Gln	Arg	Thr	Gly	Asn	Arg	His	Asp	Leu	Ala	Val	Glu	Pro	Pro	Ala	Pro	
225					230					235					240	
acc	gtg	ctg	cag	aaa	ctg	gtt	gat	gaa	aaa	cac	ggc	cag	gtg	gtt	tct	768
Thr	Val	Leu	Gln	Lys	Leu	Val	Asp	Glu	Lys	His	Gly	Gln	Val	Val	Ser	
				245					250					255		
gtc	ggg	aaa	att	gcg	gac	atc	tac	gcc	aac	tgc	ggg	atc	acc	aaa	aaa	816
Val	Gly	Lys	Ile	Ala	Asp	Ile	Tyr	Ala	Asn	Cys	Gly	Ile	Thr	Lys	Lys	
			260					265					270			
gtg	aaa	gcg	act	ggc	ctg	gac	gcg	ctg	ttt	gac	acc	acc	atc	aaa	gag	864
Val	Lys	Ala	Thr	Gly	Leu	Asp	Ala	Leu	Phe	Asp	Thr	Thr	Ile	Lys	Glu	
		275					280					285				
atg	aaa	gaa	gcg	ggg	gat	aac	acc	atc	gtc	ttc	acc	aac	ttc	gtt	gac	912
Met	Lys	Glu	Ala	Gly	Asp	Asn	Thr	Ile	Val	Phe	Thr	Asn	Phe	Val	Asp	
	290					295					300					
ttc	gac	tct	tcc	tgg	ggc	cac	cgt	cgc	gac	gtc	gcc	ggg	tat	gcc	gcg	960
Phe	Asp	Ser	Ser	Trp	Gly	His	Arg	Arg	Asp	Val	Ala	Gly	Tyr	Ala	Ala	
305					310					315					320	

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ggt ctg gaa ctg ttc gac cgc cgt ctg ccg gag ctg atg tct ctg ctg 1008
 Gly Leu Glu Leu Phe Asp Arg Arg Leu Pro Glu Leu Met Ser Leu Leu
 325 330 335

cgc gat gac gac atc ctg atc ctc acc gct gac cac ggt tgc gat ccg 1056
 Arg Asp Asp Asp Ile Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro
 340 345 350

acc tgg acc ggt act gac cac acg cgt gaa cac att ccg gta ctg gta 1104
 Thr Trp Thr Gly Thr Asp His Thr Arg Glu His Ile Pro Val Leu Val
 355 360 365

tat ggc ccg aaa gta aaa ccg ggc tca ctg ggt cat cgt gaa acc ttc 1152
 Tyr Gly Pro Lys Val Lys Pro Gly Ser Leu Gly His Arg Glu Thr Phe
 370 375 380

gcg gat atc ggc cag act ctg gca aaa tat ttt ggt act tct gat atg 1200
 Ala Asp Ile Gly Gln Thr Leu Ala Lys Tyr Phe Gly Thr Ser Asp Met
 385 390 395 400

gaa tat ggc aaa gcc atg ttc tga 1224
 Glu Tyr Gly Lys Ala Met Phe
 405

<210> 18

<211> 407

<212> PRT

<213> Escherichia coli

<400> 18

Met Lys Arg Ala Phe Ile Met Val Leu Asp Ser Phe Gly Ile Gly Ala
 1 5 10 15

Thr Glu Asp Ala Glu Arg Phe Gly Asp Val Gly Ala Asp Thr Leu Gly
 20 25 30

His Ile Ala Glu Ala Cys Ala Lys Gly Glu Ala Asp Asn Gly Arg Lys
 35 40 45

Gly Pro Leu Asn Leu Pro Asn Leu Thr Arg Leu Gly Leu Ala Lys Ala
 50 55 60

His Glu Gly Ser Thr Gly Phe Ile Pro Ala Gly Met Asp Gly Asn Ala
 65 70 75 80

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Glu Val Ile Gly Ala Tyr Ala Trp Ala His Glu Met Ser Ser Gly Lys	85	90	95
Asp Thr Pro Ser Gly His Trp Glu Ile Ala Gly Val Pro Val Leu Phe	100	105	110
Glu Trp Gly Tyr Phe Ser Asp His Glu Asn Ser Phe Pro Gln Glu Leu	115	120	125
Leu Asp Lys Leu Val Glu Arg Ala Asn Leu Pro Gly Tyr Leu Gly Asn	130	135	140
Cys His Ser Ser Gly Thr Val Ile Leu Asp Gln Leu Gly Glu Glu His	145	150	155
Met Lys Thr Gly Lys Pro Ile Phe Tyr Thr Ser Ala Asp Ser Val Phe	165	170	175
Gln Ile Ala Cys His Glu Glu Thr Phe Gly Leu Asp Lys Leu Tyr Glu	180	185	190
Leu Cys Glu Ile Ala Arg Glu Glu Leu Thr Asn Gly Gly Tyr Asn Ile	195	200	205
Gly Arg Val Ile Ala Arg Pro Phe Ile Gly Asp Lys Ala Gly Asn Phe	210	215	220
Gln Arg Thr Gly Asn Arg His Asp Leu Ala Val Glu Pro Pro Ala Pro	225	230	235
Thr Val Leu Gln Lys Leu Val Asp Glu Lys His Gly Gln Val Val Ser	245	250	255
Val Gly Lys Ile Ala Asp Ile Tyr Ala Asn Cys Gly Ile Thr Lys Lys	260	265	270
Val Lys Ala Thr Gly Leu Asp Ala Leu Phe Asp Thr Thr Ile Lys Glu	275	280	285
Met Lys Glu Ala Gly Asp Asn Thr Ile Val Phe Thr Asn Phe Val Asp	290	295	300
Phe Asp Ser Ser Trp Gly His Arg Arg Asp Val Ala Gly Tyr Ala Ala	305	310	315
			320

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Gly Leu Glu Leu Phe Asp Arg Arg Leu Pro Glu Leu Met Ser Leu Leu
 325 330 335

Arg Asp Asp Asp Ile Leu Ile Leu Thr Ala Asp His Gly Cys Asp Pro
 340 345 350

Thr Trp Thr Gly Thr Asp His Thr Arg Glu His Ile Pro Val Leu Val
 355 360 365

Tyr Gly Pro Lys Val Lys Pro Gly Ser Leu Gly His Arg Glu Thr Phe
 370 375 380

Ala Asp Ile Gly Gln Thr Leu Ala Lys Tyr Phe Gly Thr Ser Asp Met
 385 390 395 400

Glu Tyr Gly Lys Ala Met Phe
 405

<210> 19

<211> 780

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) .. (777)

<400> 19

atg act gat ctg aaa gca agc agc ctg cgt gca ctg aaa ttg atg gac 48
 Met Thr Asp Leu Lys Ala Ser Ser Leu Arg Ala Leu Lys Leu Met Asp
 1 5 10 15

ctg aac acc ctg aat gac gac gac acc gac gag aaa gtg atc gcc ctg 96
 Leu Asn Thr Leu Asn Asp Asp Asp Thr Asp Glu Lys Val Ile Ala Leu
 20 25 30

tgt cat cag gcc aaa act ccg gtc ggc aat acc gcc gct atc tgt atc 144
 Cys His Gln Ala Lys Thr Pro Val Gly Asn Thr Ala Ala Ile Cys Ile
 35 40 45

tat cct cgc ttt atc ccg att gct cgc aaa act ctg aaa gag cag ggc 192
 Tyr Pro Arg Phe Ile Pro Ile Ala Arg Lys Thr Leu Lys Glu Gln Gly
 50 55 60

acc ccg gaa atc cgt atc gct acg gta acc aac ttc cca cac ggt aac	240
Thr Pro Glu Ile Arg Ile Ala Thr Val Thr Asn Phe Pro His Gly Asn	
65 70 75 80	
gac gac atc gac atc gcg ctg gca gaa acc cgt gcg gca atc gcc tac	288
Asp Asp Ile Asp Ile Ala Leu Ala Glu Thr Arg Ala Ala Ile Ala Tyr	
85 90 95	
ggc gct gat gaa gtt gac gtt gtg ttc ccg tac cgc gcg ctg atg gcg	336
Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala	
100 105 110	
ggc aac gag cag gtt ggt ttt gac ctg gtg aaa gcc tgt aaa gag gct	384
Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala	
115 120 125	
tgc gcg gca gcg aat gta ctg ctg aaa gtg atc atc gaa acc ggc gaa	432
Cys Ala Ala Ala Asn Val Leu Leu Lys Val Ile Ile Glu Thr Gly Glu	
130 135 140	
ctg aaa gac gaa gcg ctg atc cgt aaa gcg tct gaa atc tcc atc aaa	480
Leu Lys Asp Glu Ala Leu Ile Arg Lys Ala Ser Glu Ile Ser Ile Lys	
145 150 155 160	
gcg ggt gtg gac ttc atc aaa acc tct acc ggt aaa gtg gct gtg aac	528
Ala Gly Val Asp Phe Ile Lys Thr Ser Thr Gly Lys Val Ala Val Asn	
165 170 175	
gcg acg ccg gaa agc gcg cgc atc atg atg gaa gtg atc cgt gat atg	576
Ala Thr Pro Glu Ser Ala Arg Ile Met Met Glu Val Ile Arg Asp Met	
180 185 190	
ggc gta gaa aaa acc gtt ggt ttc aaa ccg gcg ggc ggc gtg cgt act	624
Gly Val Glu Lys Thr Val Gly Phe Lys Pro Ala Gly Gly Val Arg Thr	
195 200 205	
gcg gaa gat gcg cag aaa tat ctc gcc att gca gat gaa ctg ttc ggt	672
Ala Glu Asp Ala Gln Lys Tyr Leu Ala Ile Ala Asp Glu Leu Phe Gly	
210 215 220	
gct gac tgg gca gat gcg cgt cac tac cgc ttt ggc gct tcc agc ctg	720
Ala Asp Trp Ala Asp Ala Arg His Tyr Arg Phe Gly Ala Ser Ser Leu	
225 230 235 240	

35/36

ctg gca agc ctg ctg aaa gcg ctg ggt cac ggc gac ggt aag agc gcc 768
 Leu Ala Ser Leu Leu Lys Ala Leu Gly His Gly Asp Gly Lys Ser Ala
 245 250 255

agc agc tac taa 780
 Ser Ser Tyr

<210> 20
 <211> 259
 <212> PRT
 <213> Escherichia coli

<400> 20
 Met Thr Asp Leu Lys Ala Ser Ser Leu Arg Ala Leu Lys Leu Met Asp
 1 5 10 15

Leu Asn Thr Leu Asn Asp Asp Asp Thr Asp Glu Lys Val Ile Ala Leu
 20 25 30

Cys His Gln Ala Lys Thr Pro Val Gly Asn Thr Ala Ala Ile Cys Ile
 35 40 45

Tyr Pro Arg Phe Ile Pro Ile Ala Arg Lys Thr Leu Lys Glu Gln Gly
 50 55 60

Thr Pro Glu Ile Arg Ile Ala Thr Val Thr Asn Phe Pro His Gly Asn
 65 70 75 80

Asp Asp Ile Asp Ile Ala Leu Ala Glu Thr Arg Ala Ala Ile Ala Tyr
 85 90 95

Gly Ala Asp Glu Val Asp Val Val Phe Pro Tyr Arg Ala Leu Met Ala
 100 105 110

Gly Asn Glu Gln Val Gly Phe Asp Leu Val Lys Ala Cys Lys Glu Ala
 115 120 125

Cys Ala Ala Ala Asn Val Leu Leu Lys Val Ile Ile Glu Thr Gly Glu
 130 135 140

Leu Lys Asp Glu Ala Leu Ile Arg Lys Ala Ser Glu Ile Ser Ile Lys
 145 150 155 160

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Ala Gly Val Asp Phe Ile Lys Thr Ser Thr Gly Lys Val Ala Val Asn
165 170 175

Ala Thr Pro Glu Ser Ala Arg Ile Met Met Glu Val Ile Arg Asp Met
180 185 190

Gly Val Glu Lys Thr Val Gly Phe Lys Pro Ala Gly Gly Val Arg Thr
195 200 205

Ala Glu Asp Ala Gln Lys Tyr Leu Ala Ile Ala Asp Glu Leu Phe Gly
210 215 220

Ala Asp Trp Ala Asp Ala Arg His Tyr Arg Phe Gly Ala Ser Ser Leu
225 230 235 240

Leu Ala Ser Leu Leu Lys Ala Leu Gly His Gly Asp Gly Lys Ser Ala
245 250 255

Ser Ser Tyr